

Determining Possible Fragments Based On Experimental Restrictions

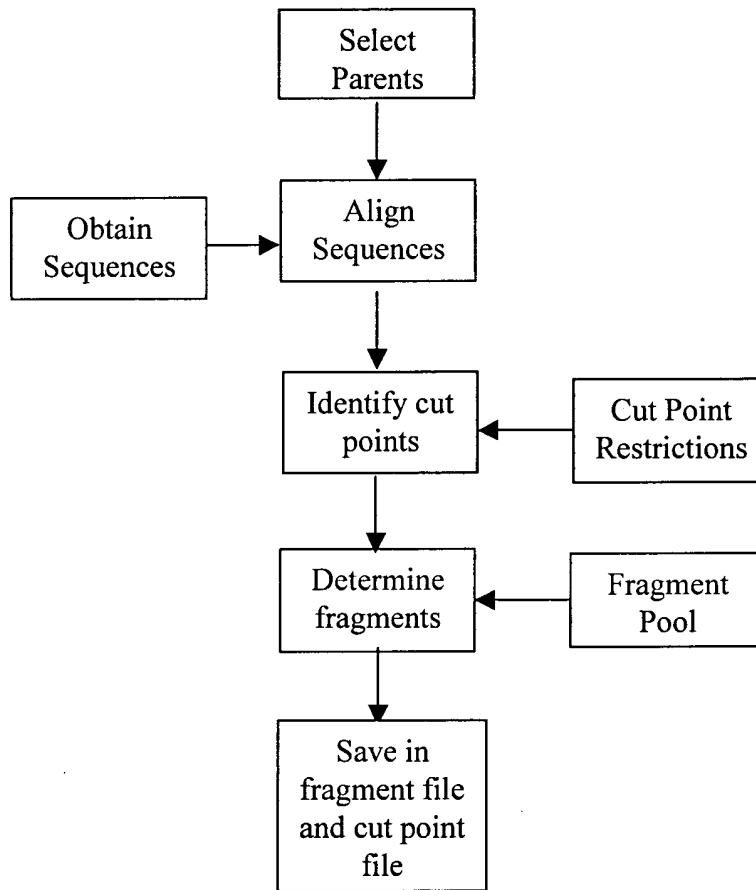


FIG. 1A

Determining the Schema Disruption Profile for a Structure

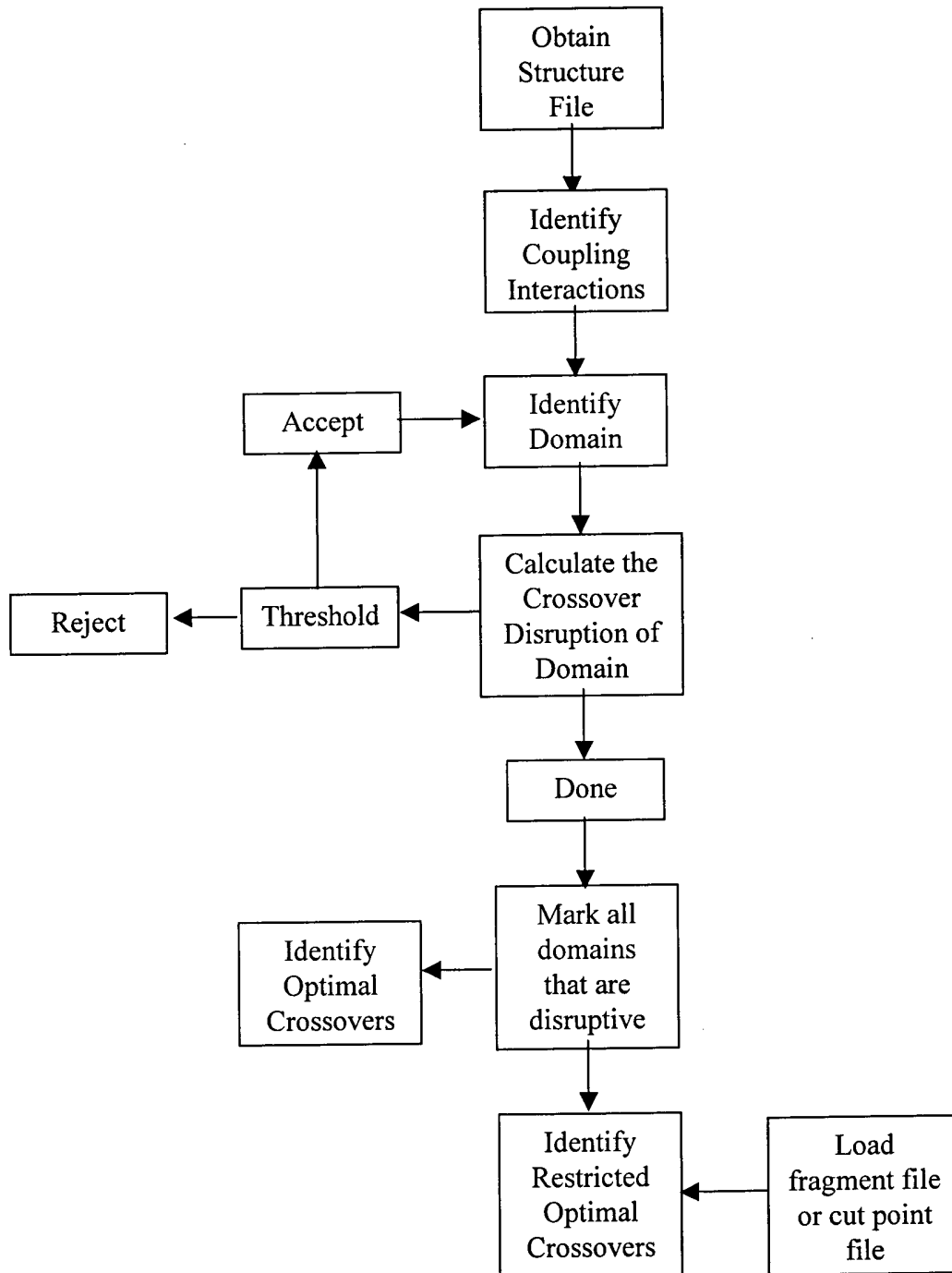


FIG. 1B

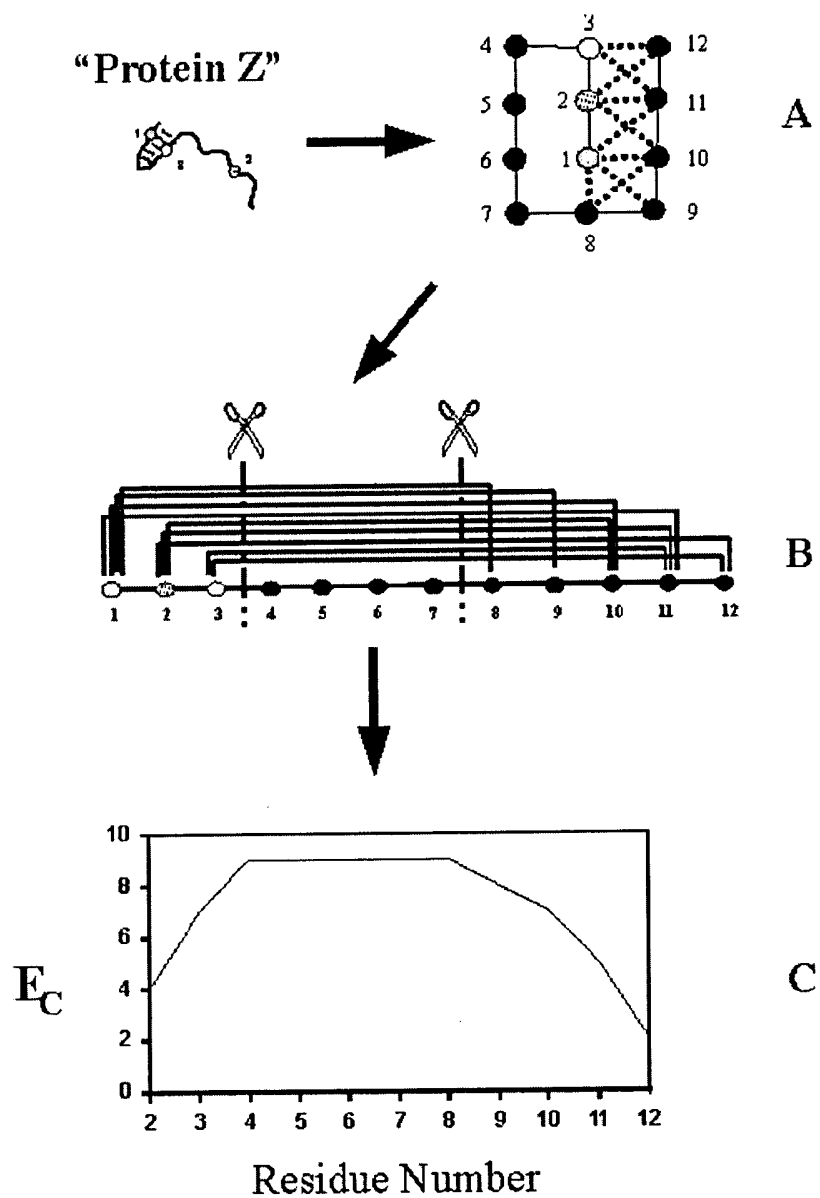


FIG. 2

1	1	T	P	V	S	E	K	O	L	A	E	V	V	A	N	T	I	T	P	L	M	K	A	Q	S	V	P	G	M	A	V	A	V	I	Y	Q	G	K	P	H	Y	T	F	G	K	A	D	I	A			
2	1	A	K	T	E	Q	Q	I	A	D	I	V	N	N	T	I	T	P	L	M	Q	E	Q	A	I	P	G	M	A	V	A	V	I	Y	E	G	K	P	Y	T	W	G	K	A	D	I	A					
3	1	T	A	K	L	T	E	L	Q	V	A	T	I	V	N	N	T	I	T	P	L	E	K	E	Q	A	I	P	G	M	A	V	A	V	I	Y	E	G	K	P	Y	T	W	G	K	A	D	I	A			
4	1	Y	A	R	G	E	A	P	L	T	A	A	V	D	G	I	I	O	P	M	L	K	E	Y	R	I	P	G	M	A	V	A	V	I	Y	D	G	K	P	Y	T	W	G	K	A	D	I	A				
1	51	N	K	P	V	T	P	Q	T	L	F	E	L	G	S	I	S	K	T	F	T	G	V	L	G	G	D	A	I	A	R	G	E	I	S	L	D	D	A	V	T	R	Y	W	P	O	L	T	G	K	Q	
2	51	N	H	P	V	T	Q	T	L	F	E	L	G	S	V	S	K	T	F	N	G	V	A	L	G	G	D	R	I	A	R	G	E	I	K	L	S	D	P	V	T	K	Y	W	P	E	L	T	G	K	Q	
3	51	G	R	P	V	T	E	Q	T	L	F	E	L	G	S	V	S	K	T	F	N	G	V	A	L	G	G	D	R	I	A	R	G	E	I	K	L	S	D	P	V	T	K	Y	W	P	E	L	T	G	K	Q
4	51	G	Q	R	V	S	E	Q	T	L	F	E	L	G	S	V	S	K	T	F	N	G	V	A	L	G	G	D	R	I	A	R	G	E	I	K	L	S	D	P	V	T	K	Y	W	P	E	L	T	G	K	Q
1	101	W	Q	G	I	R	M	L	D	L	A	T	Y	T	A	G	G	L	P	L	Q	V	P	D	E	V	T	D	N	A	S	L	L	R	F	Y	Q	N	W	Q	P	Q	W	K	P	G	T	R	L	Y		
2	101	W	R	G	I	S	L	H	L	A	T	Y	T	A	G	G	L	P	L	Q	I	P	G	D	V	T	D	K	A	E	L	L	R	F	Y	Q	N	W	Q	P	Q	W	T	P	G	A	K	R	L	Y		
3	101	W	K	D	V	K	M	L	H	L	A	T	Y	T	A	G	G	L	P	L	Q	I	P	D	S	V	T	D	Q	K	S	L	W	Q	Y	Q	Q	W	Q	P	Q	W	A	P	G	V	M	R	N	Y		
4	101	F	D	G	V	T	M	A	E	L	A	T	Y	S	A	G	G	L	P	L	Q	F	P	D	E	V	D	S	N	D	K	M	R	T	Y	R	H	W	S	P	V	Y	P	A	G	T	H	R	Q	Y		
1	151	A	N	A	S	I	G	L	F	G	A	L	A	V	K	P	S	G	M	P	Y	E	Q	A	M	T	R	V	L	K	P	L	K	L	D	H	T	W	I	N	V	P	K	A	E	E	A	H	Y	A		
2	151	A	N	S	I	G	L	F	G	A	L	A	V	K	P	S	G	M	P	Y	E	Q	A	M	T	R	V	L	K	P	L	K	L	D	H	T	W	I	N	V	P	K	A	E	E	A	H	Y	A			
3	151	S	N	A	S	I	G	L	F	G	A	L	A	V	K	P	S	G	M	P	Y	E	Q	A	M	T	R	V	L	K	P	L	K	L	D	H	T	W	I	N	V	P	K	A	E	E	A	H	Y	A		
4	151	S	N	P	S	I	G	L	F	G	H	L	A	A	N	S	L	G	Q	P	F	E	Q	L	M	S	Q	T	L	L	P	K	L	G	L	H	T	Y	I	Q	V	P	E	S	A	I	A	L	K	T		
1	201	W	G	Y	R	D	G	K	A	V	R	V	S	P	G	M	L	D	A	O	A	Y	G	V	K	T	N	V	Q	D	M	A	N	W	V	M	A	N	M	A	P	E	N	V	A	D	A	S	L	K	Q	
2	201	W	G	Y	L	E	G	K	P	V	H	V	S	P	G	M	L	D	A	E	A	Y	G	V	K	S	S	V	I	D	M	A	R	W	V	Q	A	N	M	D	P	E	S	L	G	N	D	K	L	K	E	
3	201	W	G	Y	K	D	G	K	P	V	H	V	T	L	G	M	L	D	A	E	A	Y	G	V	K	S	S	V	I	D	M	A	R	W	V	Q	A	N	M	D	P	E	S	L	G	N	D	K	L	K	E	
4	201	Y	G	Y	K	E	D	K	P	V	R	V	T	P	G	V	L	A	A	E	A	Y	G	I	K	T	G	S	A	D	L	L	K	F	T	E	A	N	M	G	Y	Q	.	.	G	D	A	A	L	K	T	
1	251	G	I	A	L	A	Q	S	R	Y	W	R	I	G	S	M	Y	Q	G	L	G	W	E	M	L	N	W	P	V	E	A	N	T	V	E	G	S	D	S	K	V	A	L	A	P	L	P	V	A	E		
2	251	A	I	E	L	A	Q	S	R	Y	W	R	I	G	S	M	Y	Q	G	L	G	W	E	M	L	N	W	P	V	E	A	N	T	V	E	G	S	D	S	K	V	A	L	A	P	L	P	V	A	E		
3	251	A	I	E	L	A	Q	S	R	Y	W	R	I	G	S	M	Y	Q	G	L	G	W	E	M	L	N	W	P	V	E	A	N	T	V	E	G	S	D	S	K	V	A	L	A	P	L	P	V	A	E		
4	249	R	I	A	L	T	H	T	G	F	Y	S	V	G	D	M	T	Q	G	L	G	W	E	S	Y	A	Y	P	L	T	N	E	Q	A	L	L	A	G	N	S	P	A	V	S	F	Q	A	N	P	V	T	
1	301	V	N	P	P	A	P	V	K	A	S	W	V	H	K	T	G	S	T	G	G	F	G	S	Y	V	A	F	I	P	E	K	Q	I	G	I	V	M	L	A	N	K	S	Y	P	N	P	A	R	V		
2	301	V	N	P	P	A	P	A	V	K	A	S	W	V	H	K	T	G	S	T	G	G	F	G	S	Y	V	A	F	I	P	E	K	Q	I	G	I	V	M	L	A	N	K	S	Y	P	N	P	A	R	V	
3	301	L	V	P	A	P	A	V	K	A	S	W	V	H	K	T	G	S	T	G	G	F	G	S	Y	V	A	F	I	P	E	K	Q	I	G	I	V	M	L	A	N	K	S	Y	P	N	P	A	R	V		
4	299	F	A	V	P	K	A	M	G	E	Q	R	L	Y	N	K	T	G	S	T	G	G	F	G	A	Y	V	A	F	I	P	E	K	Q	I	A	I	V	M	L	A	N	K	N	Y	P	I	E	A	R	V	
1	351	E	A	A	Y	H	I	L	E	A	L	L	Q																																							
2	351	K	A	A	W	R	I	L	E	K	L	Q																																								
3	351	Q	A	A	Y	D	I	L	Q	A	L	R																																								
4	349	K	A	A	H	A	I	L	S	O	L	A																																								

1	Enterbacter cloacae	P05364 (X03866)
2	Citrobacter freundii	P05193 (X07274)
3	Yersinia enterocolitica	P45460 (X63149)
4	Klebsiella pneumoniae	Q48437 (X77455)

FIG. 3

Figure 1 is a line graph showing the probability of crossover ($P(\text{crossover})$) versus Residue Number for the protein P1. The y-axis ranges from 0.00 to 0.06, and the x-axis ranges from 0 to 350. The graph shows several peaks, with the highest peak at residue 60 ($P(\text{crossover}) \approx 0.06$). Other significant peaks are at residues 25, 125, 275, and 325. Horizontal bars below the x-axis indicate regions of high probability of crossover.

FIG. 4B

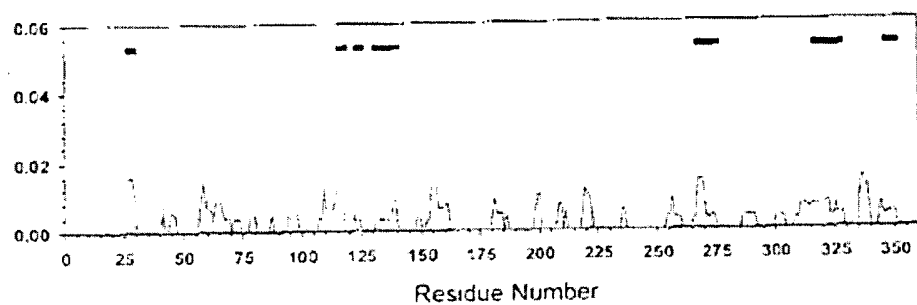


FIG. 4C

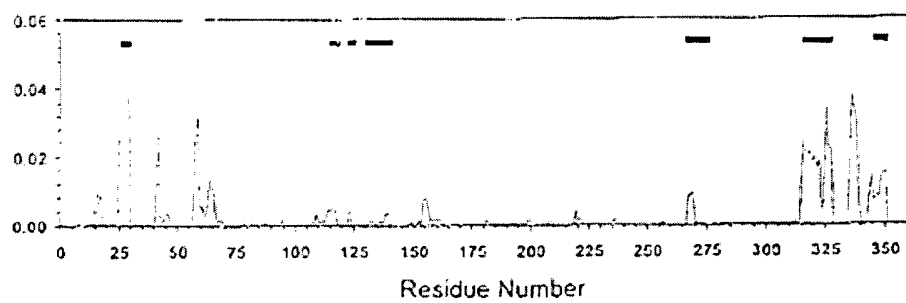


FIG. 4D

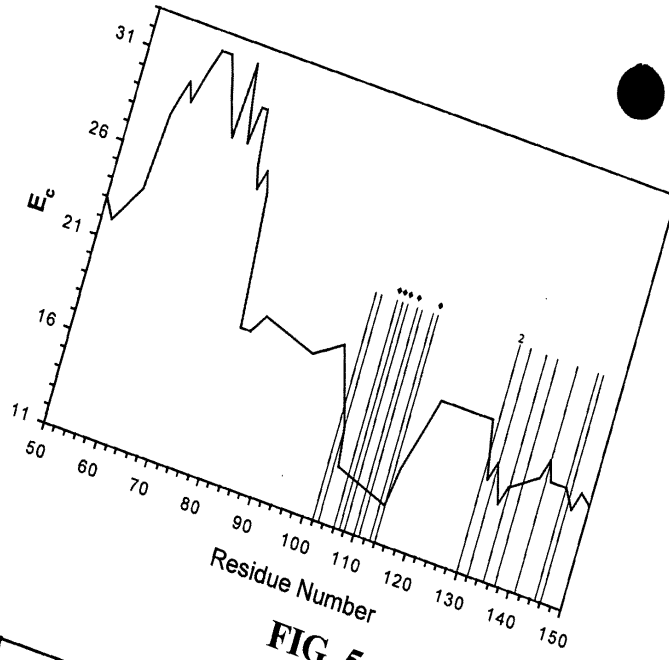


FIG. 5

00637-0527
T0E250-594E9660

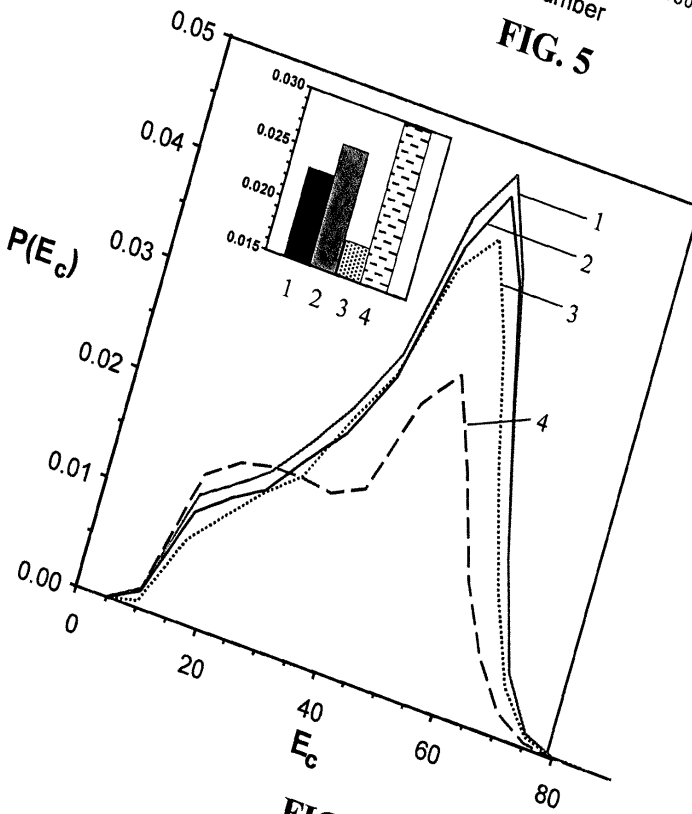
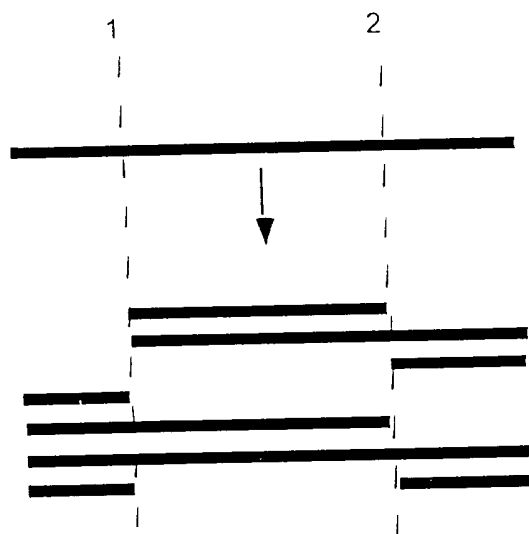


FIG. 6



09863765-100101

(A)



(B)

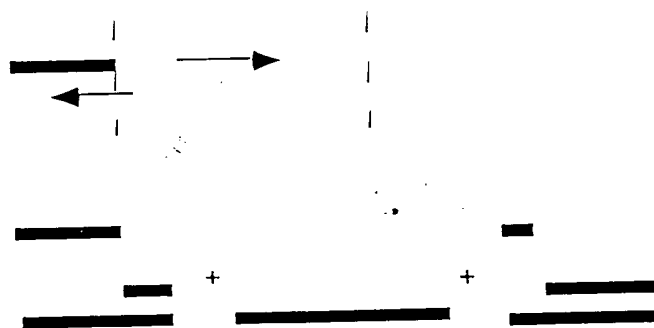


FIG. 7

09853765-100101

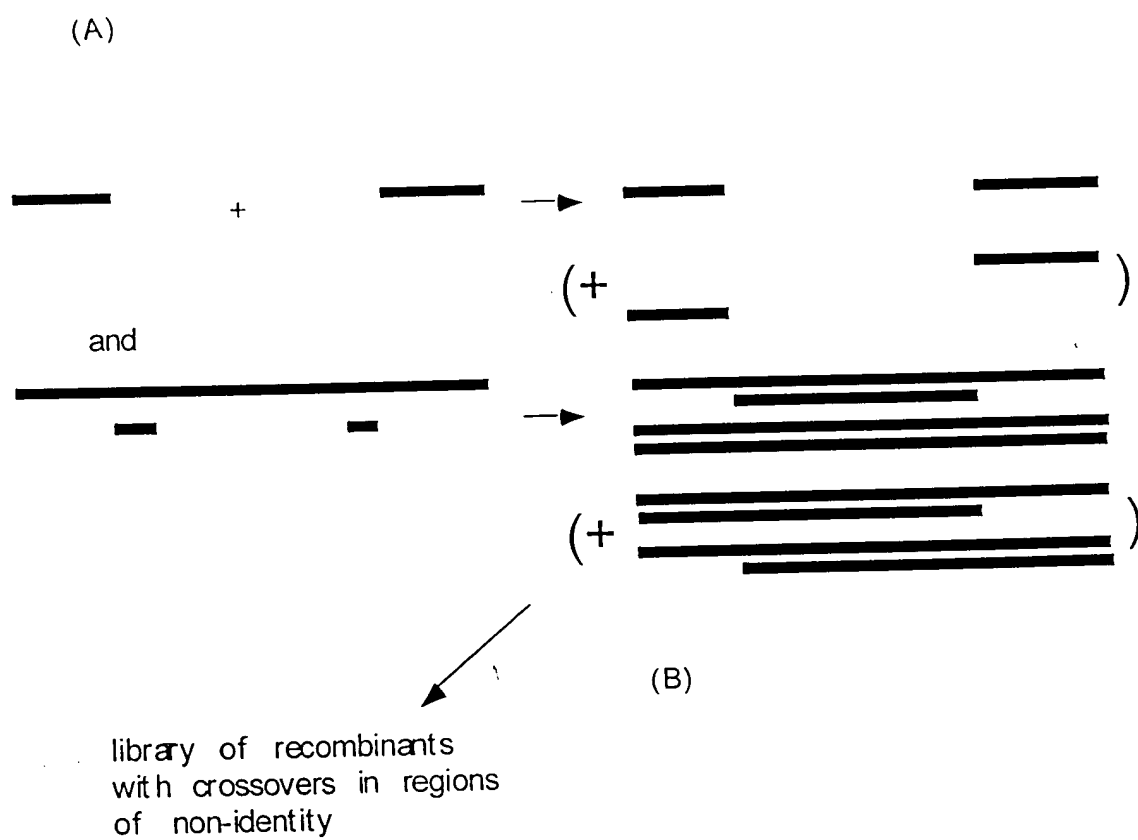
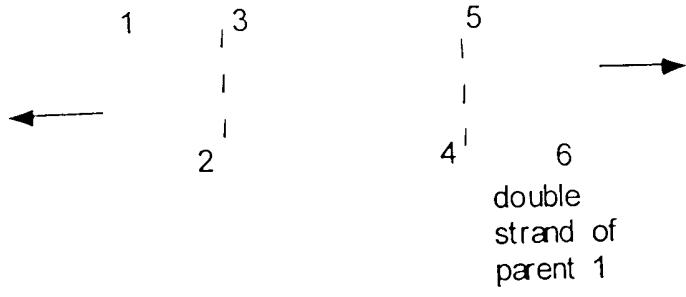


FIG. 8



(A)

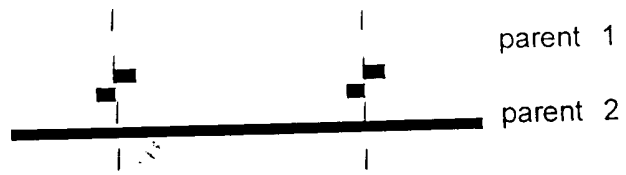


(B)

Reassemble fragments in a pool, by PCR with 1+ 6

FIG. 9

(A)



(B)



FIG. 10

09663763-100101

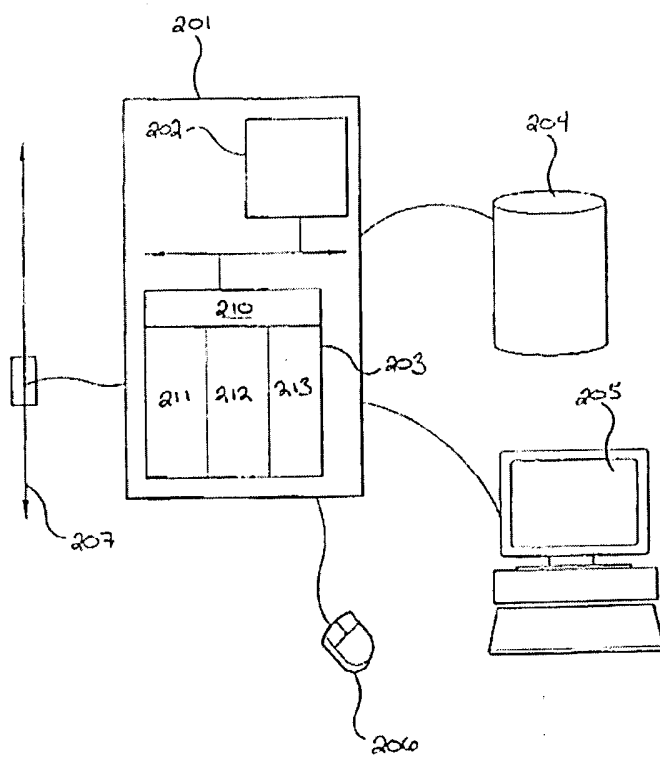


FIG. 11

Récombinant search algorithm

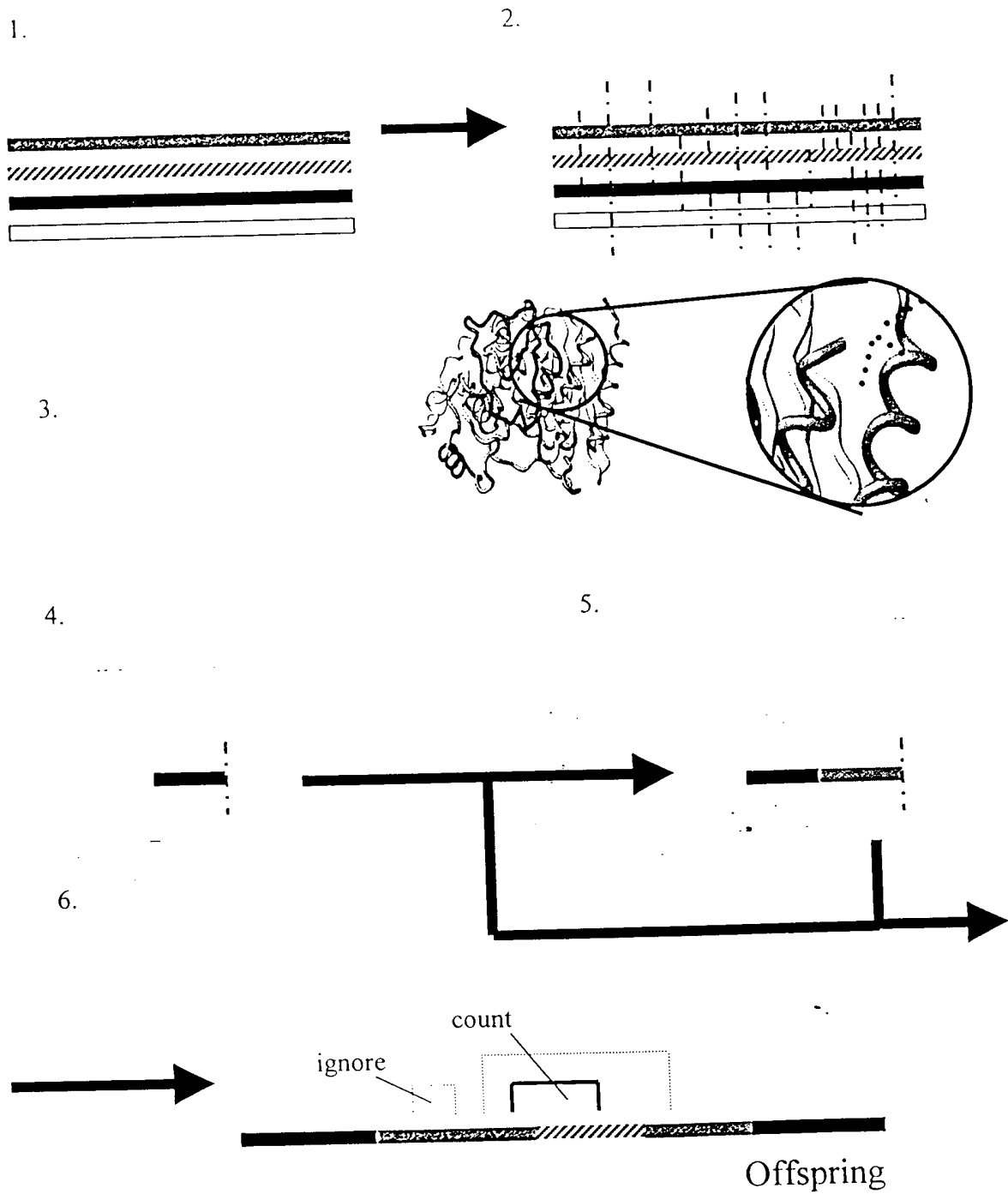


FIG. 12

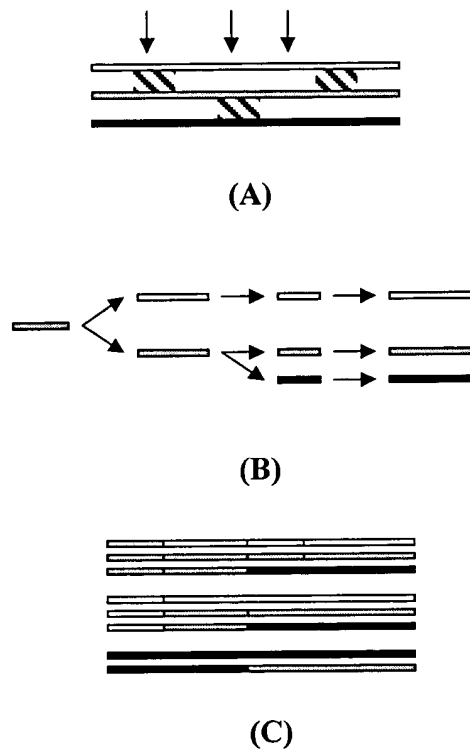


FIG. 13

DIRECTED EVOLUTION ALGORITHM

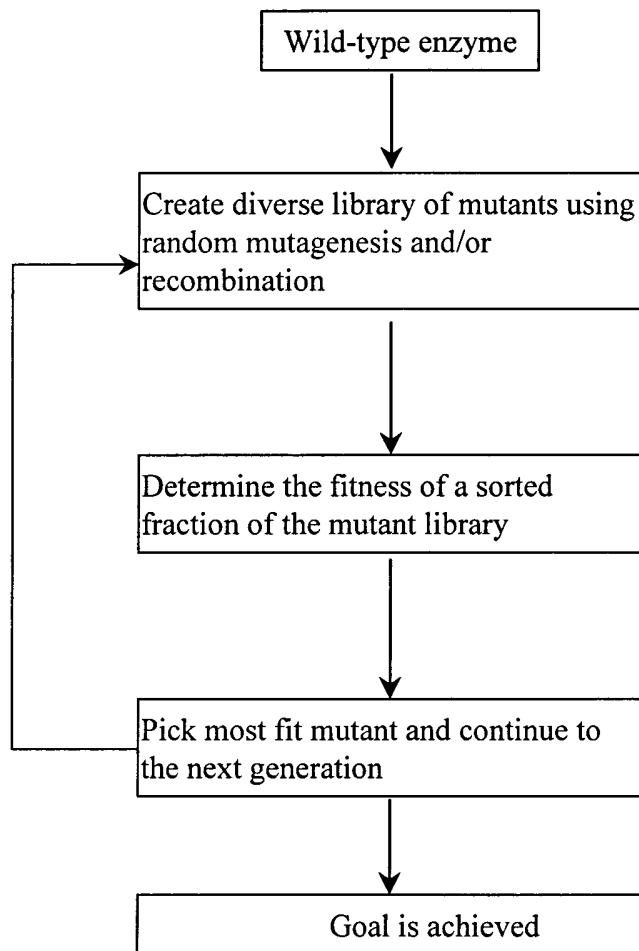


FIG. 14

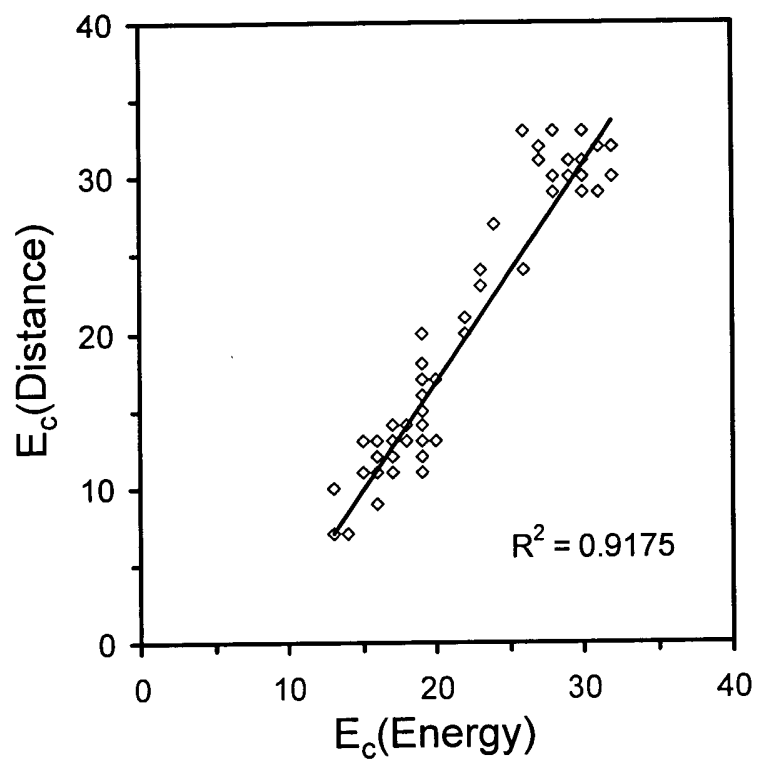


FIG. 15

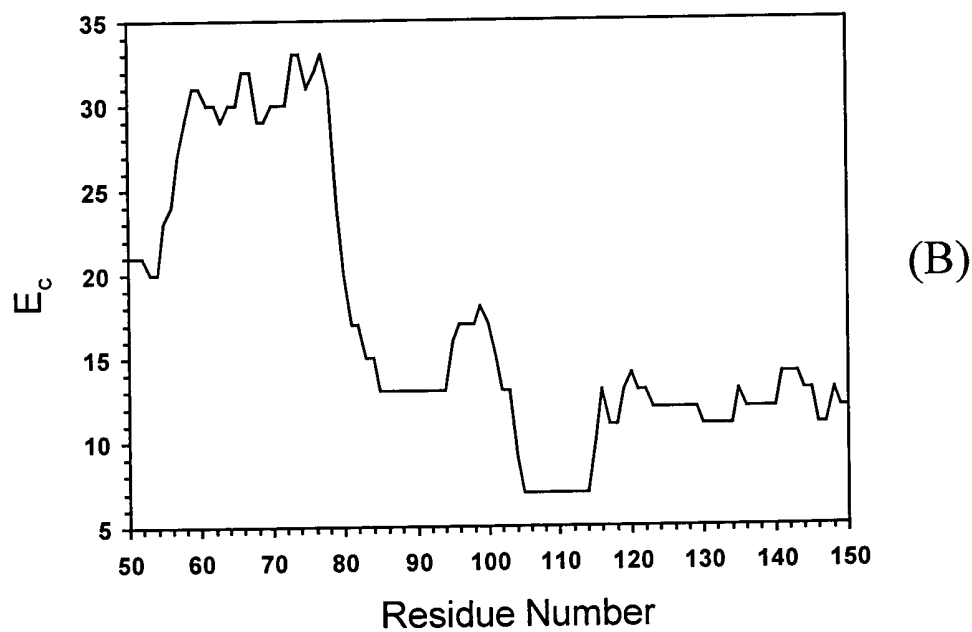
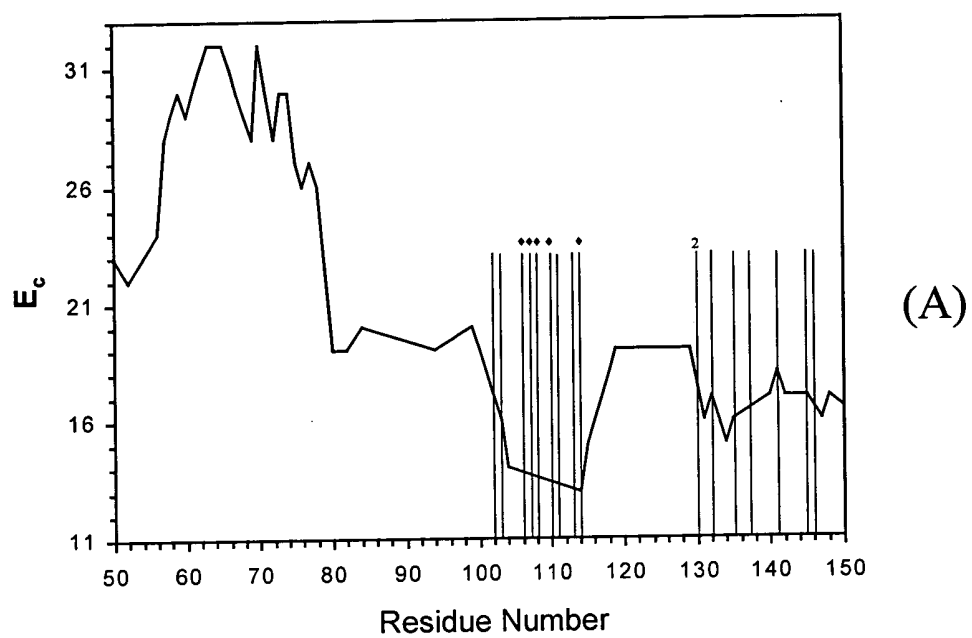


FIG. 16



(A)

Experimental Data:

	wt	wt-insert	1	2
Tm(dC)	52	55.2	n.d.	54.3
Tm(dC)	49.5	53.3	44.5	52.5
t1/2	12.1	2586	-	87.5
t1/2	53	138	4	308

(B)

Calculations:

	All schema		Fragments		Z-score	
	av	stdev	1	2	1	2
Ec	19.260	4.090	10.770	8.124	-2.076	-2.723
Ec*	0.006	0.002	0.014	0.005	4.838	-0.857

FIG. 17

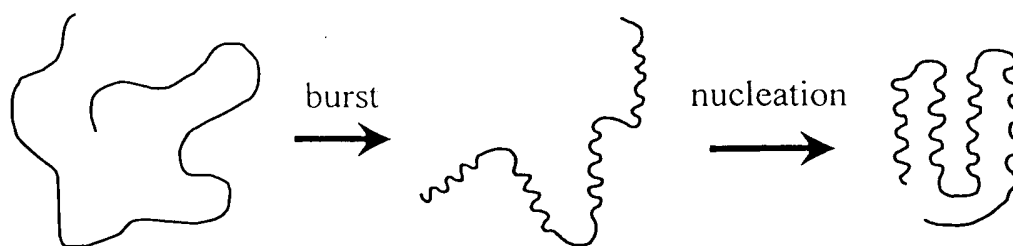


FIG. 18

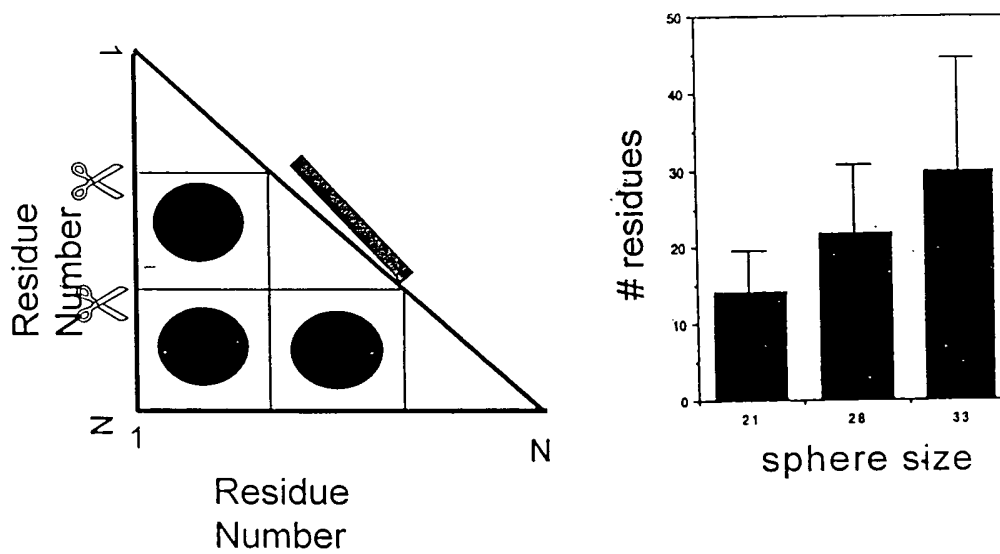


FIG. 19

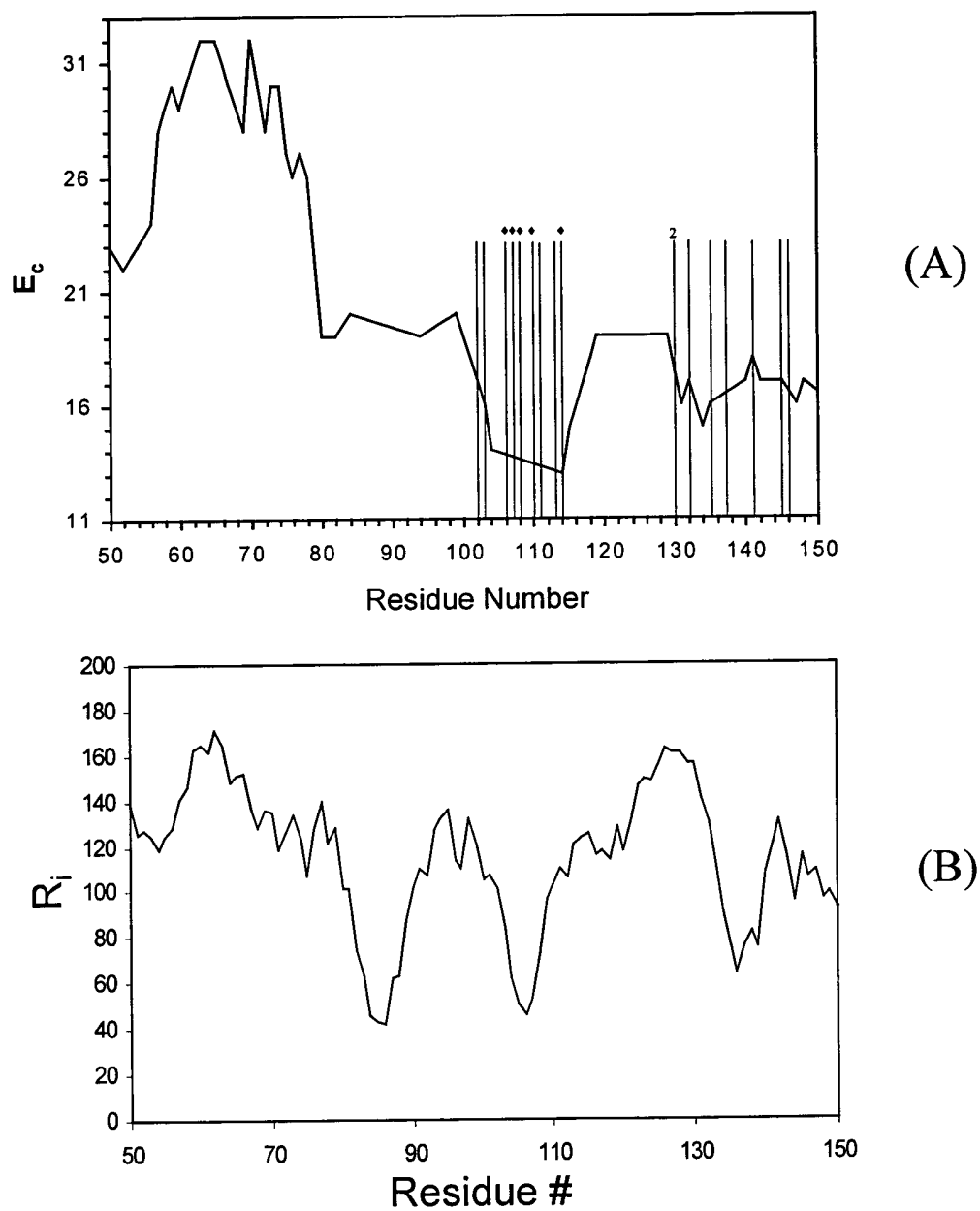


FIG. 20

FOE250"597E9860

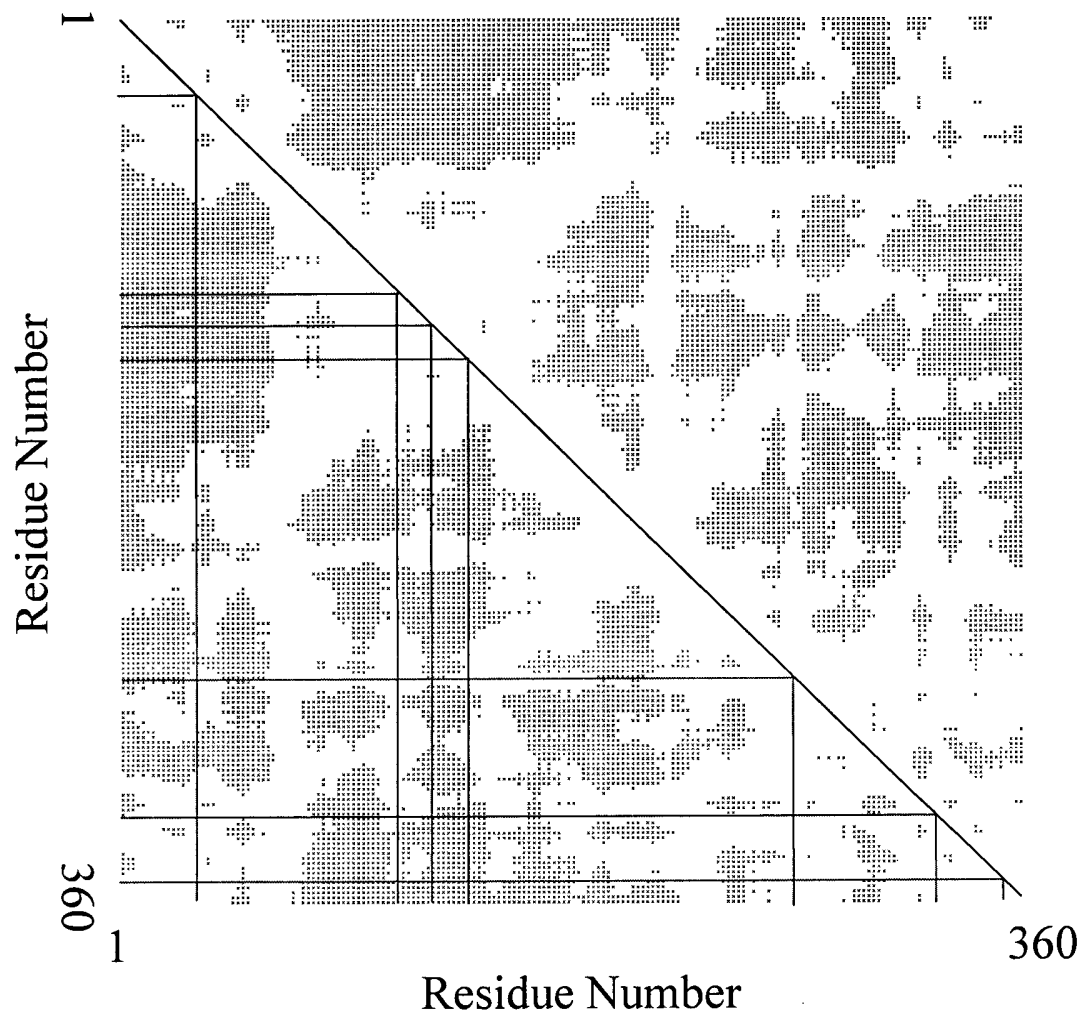


FIG. 21

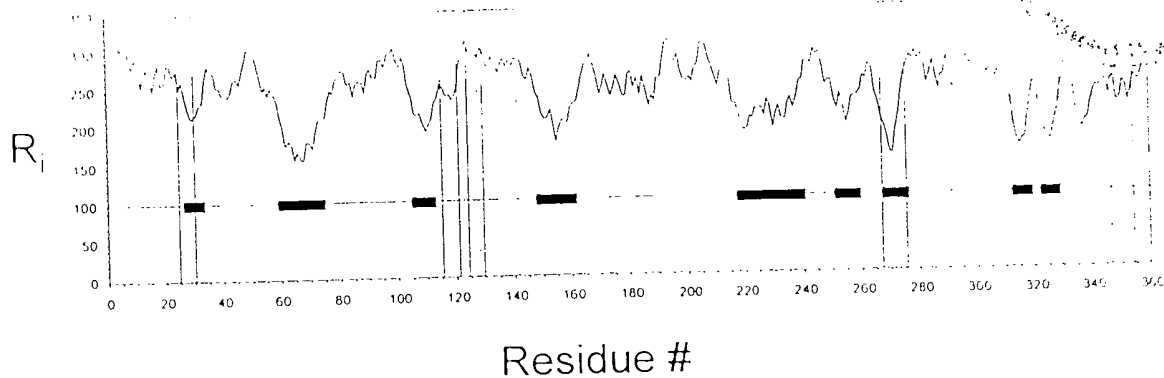


FIG. 22

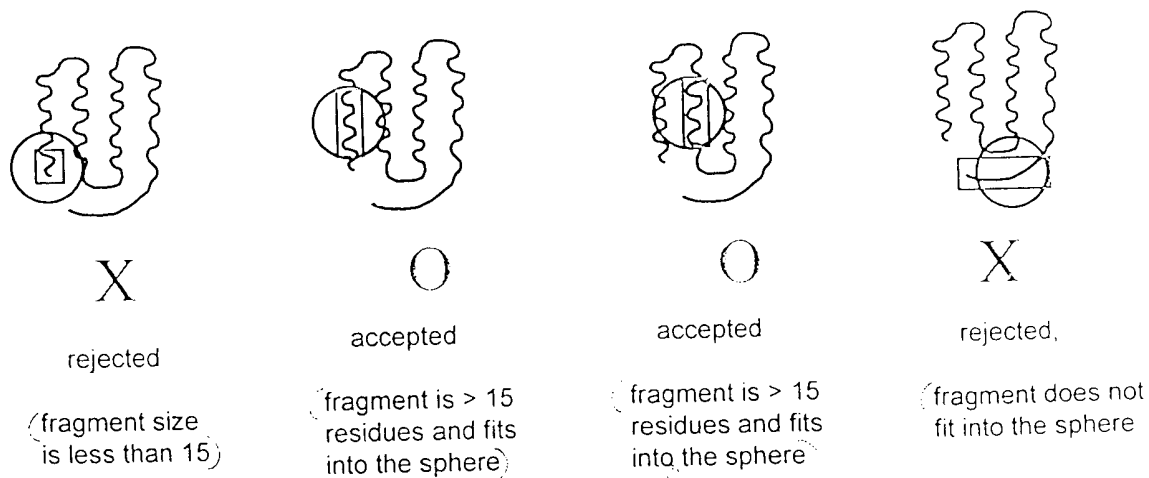


FIG. 23

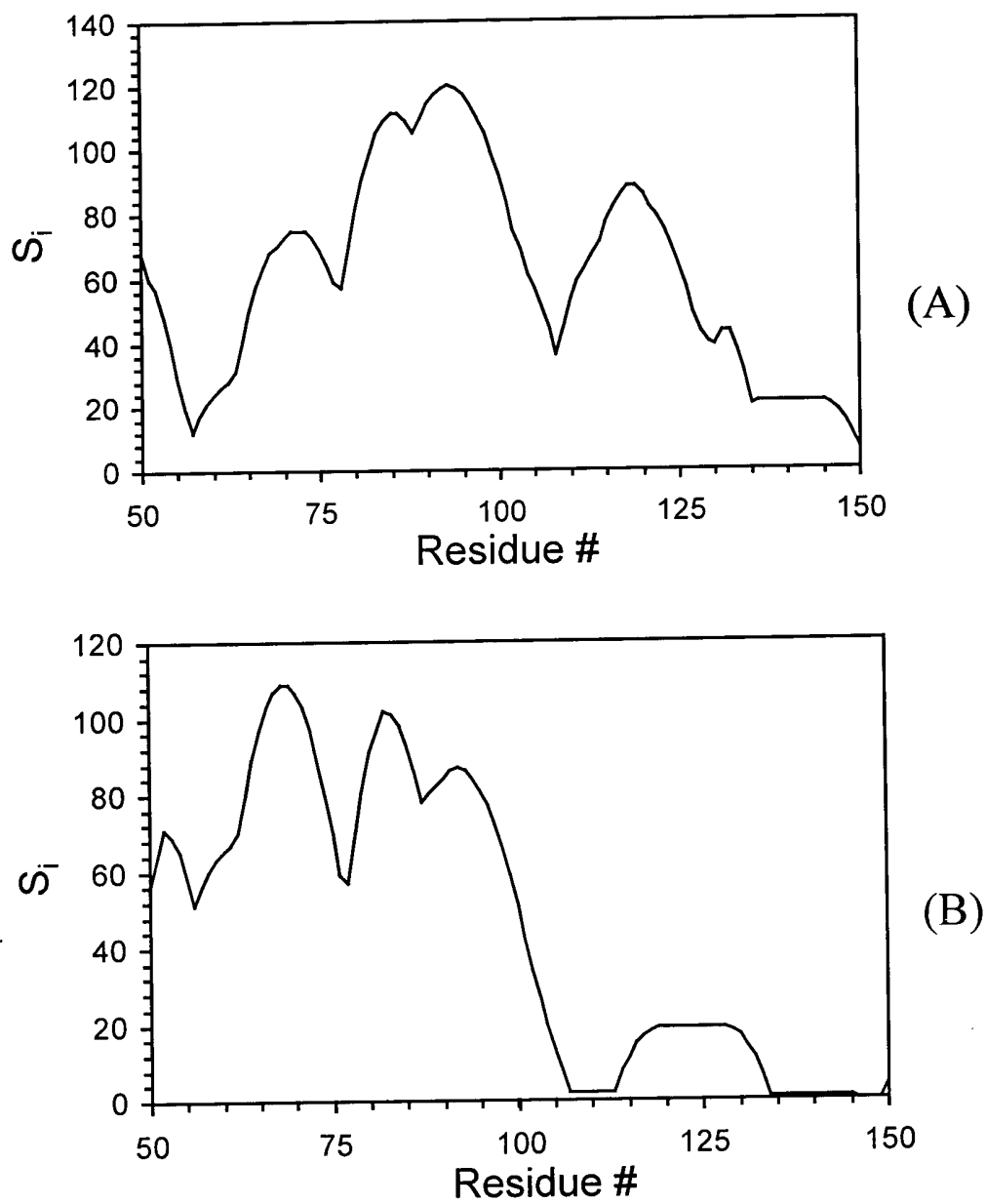


FIG. 24

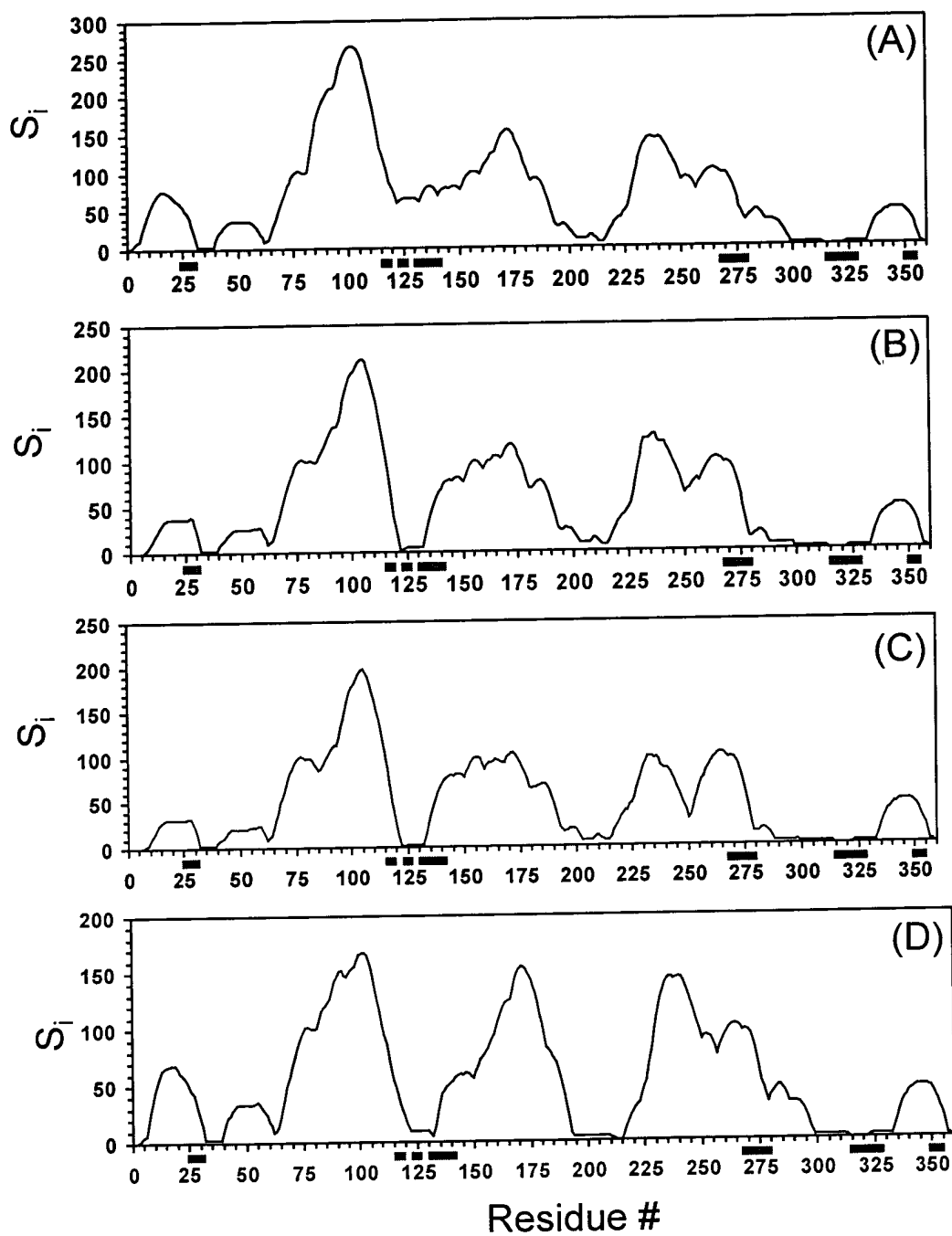


FIG. 25

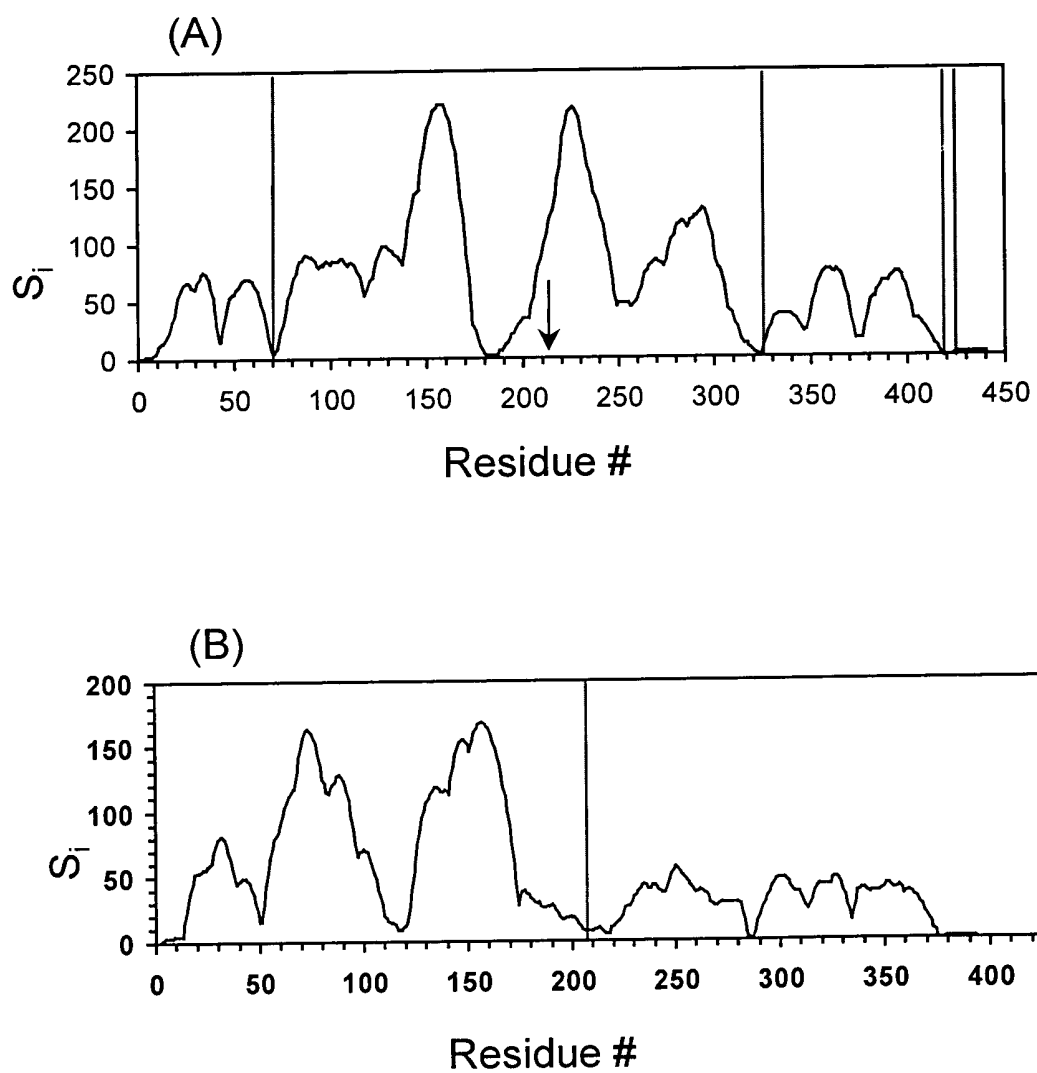


FIG. 26

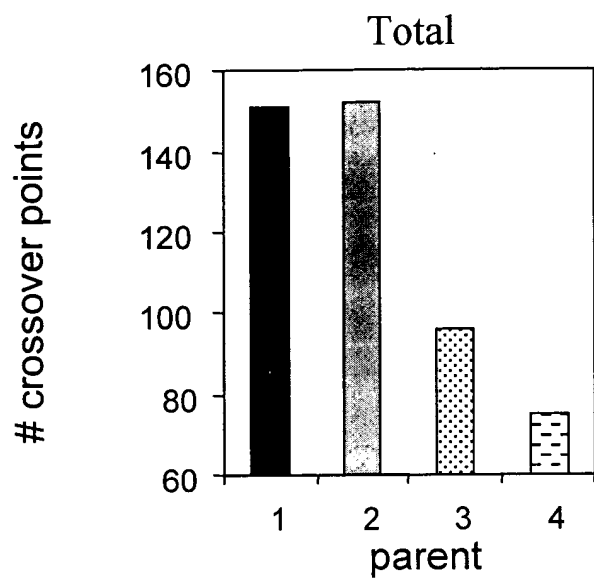


FIG. 27A

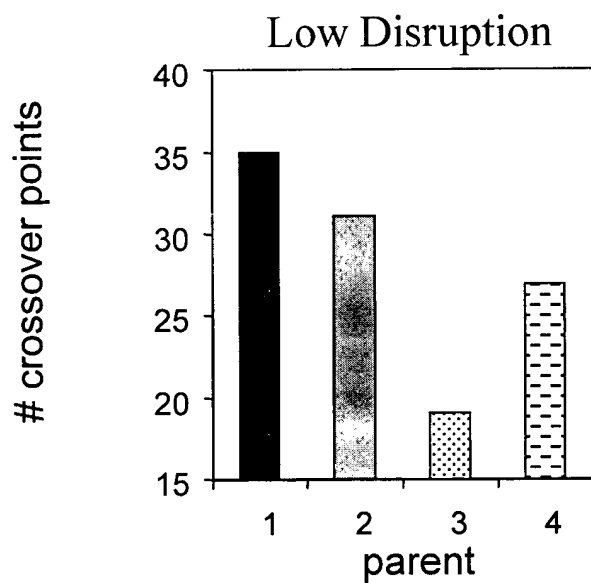


FIG. 27B